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1: Protein Sci. 1998 Nov;7(11):2359-73.

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pH-induced conformational changes of membrane-bound influenza hemagglutinin and its effect on target lipid bilayers.

Gray C, Tamm LK.

Department of Molecular Physiology and Biological Physics, University of Virginia Health Sciences Center, Charlottesville 22906-0011, USA.

Influenza virus hemagglutinin (HA) has served as a paradigm for both pH-dependent and -independent viral membrane fusion. Although large conformational changes were observed by X-ray crystallography when soluble fragments of HA were subjected to fusion-pH conditions, it is not clear whether the same changes occur in membrane-bound HA, what the spatial relationship is between the conformationally changed HA and the target and viral membranes, and in what way HA perturbs the target membrane at low pH. We have taken a spectroscopic approach using an array of recently developed FTIR techniques to address these questions. Difference attenuated total reflection FTIR spectroscopy was employed to reveal reversible and irreversible components of the pH-induced conformational change of the membrane-bound bromelain fragment of HA, BHA. Additional proteolytic fragments of BHA were produced which permitted a tentative assignment of the observed changes to the HA1 and HA2 subunits, respectively. The membrane-bound HA1 subunit undergoes a reversible conformational change, which most likely involves the loss of a small proportion of beta-sheet at low pH. BHA was found to undergo a partially reversible tilting motion relative to the target membrane upon exposure to pH 5, indicating a previously undescribed hinge near the anchoring point to the target membrane. Time-resolved amide H/D exchange experiments revealed a more dynamic (tertiary) structure of membrane-bound BHA and its HA2, but not its HA1, subunit. Finally BHA and, to a lesser degree, HA1 perturbed the lipid bilayer of the target membrane at the interface, as assessed by spectral changes of the lipid ester carbonyl groups. These results are discussed in the context of a complementary study of HA that was bound to viral membranes through its transmembrane peptide (Gray C, Tamm LK, 1997, Protein Sci 6:1993-2006). A distinctive role for the HA1 subunit in the conformational change of HA becomes apparent from these combined studies.

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